ABSTRACT

Breast cancer is the major type of cancer in women worldwide and the second leading cause of death too. The current study was conducted to identify and evaluate *ERG* and its isoforms expression in breast cancer and to correlate the expression of *ERG* isoforms in breast cancer progression. Breast adenocarcinoma cell line MDA-MB-231, primary HUVECs and breast tumor tissues were used. Histological examination of tissue samples was done by Hematoxylin and Eosin staining. The results showed that one tissue sample (S2) was invasive lobular carcinoma (ILC) at stage IIA and the other (S3) was found to be invasive ductal carcinoma (IDC) stage IIIB. To analyze the expression of different isoforms of *ERG* quantitative PCR was performed. For this purpose isoform specific primers were designed. After extraction of RNA from cell lines and tumor tissues qPCR was performed and analysed by LinReg software and Pfaffl equation. The results showed that *ERG* isoforms *1, 2, 3, 4, 5* and *8* with highest expression of ERG3 were expressed under normal conditions in primary HUVECs while *ERG6* and *7* were totally absent. In MDA-MB-231 cell line, the expression of *ERG* isoform *3, 7 and 8* was considerable while all other isoforms were not detected. When the differential expression of *ERG* isoforms was observed it showed that the expression of *ERG* isoforms was found variable in normal breast tissue and tumor samples. In normal breast tissue *ERG1* and *3* were detected. However, in breast tumors of IDC, *ERG* isoform *3* and *8* were present while in case of ILC along with *3*, and *8* *ERG* isoform *2* was also found. It can be concluded that almost all *ERG* isoforms expressed normally in endothelial cells. However, in cancerous cells, various *ERG* isoforms were not expressed indicating that the expression of transcriptionally active isoforms in the absence of other isoforms may target the potential genes involved in progression of cell growth or regulation of anti-apoptotic pathway which play role in the development of breast cancer. Similarly, in tumor tissue samples, high expression of *ERG8* in both IDC and ILC may be involved in inhibiting the expression of other isoforms like *ERG1* that normally expressed in normal breast tissue and results into disparity of transcriptional activity of expressed isoforms. This disparity may involve in reduction of apoptotic phenotype or proliferation of cancerous cells.